IN THE CLAIMS:

Please cancel claims 30-33, 40-41 and 45-46, without prejudice or disclaimer.

Please amend claim 34 as follows:

-- 34 [Amended]. The method of claim [31] 47, wherein said method additionally includes the steps:

(E) comparing each of said [interrogated] identified single nucleotide polymorphisms of said target human, with a corresponding single nucleotide polymorphism of a reference human, and determining whether said polymorphisms contain the same single nucleotide at their respective polymorphic sites; and

(F) using said comparison to determine the extent of genetic similarity between said target human and said reference human. --

Please amend claim 35 as follows:

-- 35 [Twice Amended]. The method of claim [31] 34, wherein in step (F), said determination is sufficient to establish that said target human and said reference human are not the same person. --

Please amend claim 36 as follows:

-- 36 [Twice Amended]. The method of claim [31] 34, wherein in step (F), said determination is sufficient to establish that said reference human is not a parent of said target human. --

Please amend claim 37 as follows:

-- 37 [Twice Amended]. The method of claim [31] 34, wherein said reference human has a trait, and said determination of step (F) is sufficient to establish that said target human also has said trait. --

Please amend claim 38 as follows:

-- 38 [Twice Amended]. The method of claim [31] 34, wherein said reference human has a first and second trait, and said determination of step (F) is sufficient to establish a genetic linkage between said traits. --

Please amend claim 42 as follows:

-- 42 [Amended]. The method of claim 37, wherein said determination of step (F) comprises the substeps:

(i) determining the identity of a single nucleotide present at a polymorphic site of a[n equine] human single nucleotide polymorphism, and being present in more than 51% of a set of reference humans;

(ii) determining whether a single nucleotide present at a polymorphic site of a corresponding single nucleotide polymorphism of said target human has the same identity as the single nucleotide present at said polymorphic site of said 51% of reference humans exhibiting said trait; and

(iii) [using said determination of substep (ii) to determine] determining whether said target human will have said [particular] trait. --

Please amend claim 45 as follows:

-- 45 [Amended]. A method for creating a genetic map of unique sequence [equine] human polymorphisms which comprises the steps:

(A) identifying at least one pair of inter-breeding reference humans, wherein each of said pairs of humans is characterized by having a first and a second reference human,

said first reference human having:

two alleles (i) and (ii), said alleles each being single nucleotide polymorphic alleles having a single nucleotide polymorphic site;

said second reference human having:

a corresponding allele (i') to said allele (i) of said first reference human, wherein said allele (i') has a single nucleotide polymorphic site, and wherein the single nucleotide present at said polymorphic site of said allele (i') differs from the single nucleotide present at the polymorphic site of said allele (i) of said first reference human, and

(B) identifying in a progeny of at least one of said pairs of inter-breeding reference humans the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (i) and (i'), and the single nucleotide present at a single nucleotide polymorphic site of a corresponding allele of said alleles (ii) and (ii'); and

(C) determining the extent of genetic linkage between said alleles (i) and (ii), to thereby create said a genetic map. –

Please add the following new claims:

--47. A method for analyzing nucleic acid of a target human by identifying the nucleotide present at at least two preselected single nucleotide polymorphic sites, wherein said method comprises:

(A) selecting said single nucleotide polymorphic sites for such analysis;

(B) hybridizing at least two primer molecules to at least one nucleic acid molecule of said target human, wherein one of said primer molecules specifically hybridizes to an invariant proximal nucleotide sequence or an invariant distal nucleotide sequence of one of said single nucleotide polymorphic sites and another of said primer molecules specifically hybridizes to another invariant proximal nucleotide sequence or invariant distal nucleotide sequence of one of said single nucleotide polymorphic sites;

(C) determining the identity of the nucleotide present at each of said selected single nucleotide polymorphic sites; and

(D) comparing the identity of said determined nucleotide present at each of said single nucleotide polymorphic sites with the identity of a reference nucleotide, said reference nucleotide being present at each of said single nucleotide polymorphic sites in a reference organism.

48. The method of claim 47, wherein said method additionally comprises identifying the presence of a genetic trait of said target human, and wherein at least one of said single nucleotide polymorphic sites is within about 150 bases of said genetic trait.

49. The method of claim 47, wherein the identity of the nucleotide present at each of said single nucleotide polymorphic sites is determined by extending each of said hybridized primer molecules under conditions sufficient to permit a polymerase-mediated, template-dependent extension of said primer molecules, said extension causing the incorporation of a single dideoxynucleotide derivative to the 3'terminus of said primer molecule, said incorporated single dideoxynucleotide derivative being complementary to the nucleotide of the polymorphic site of said single nucleotide polymorphism.

50. A method for determining whether a target human possesses a mutation linked to a genetic trait, said method comprising the steps:

(A) amplifying nucleic acid of said target human, wherein said nucleic acid contains at least one single nucleotide polymorphism and wherein said single nucleotide polymorphism is within about 150 bases of said mutation linked to said genetic trait;